Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	0	"wolffe.in"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L2	67	wolffe.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L3	33	L2 and "chromatin"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L4	9944	cox.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L5	22	L4 and "zinc finger"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L6	6	"6453242".pn. or "6534261".pn. or "6503717".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L7	67	wolffe.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L8	33	L7 and "chromatin"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L9	9944	cox.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L10	160	collingwood.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L11	506	sangamo$.as.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43

L12	143891	"methyl transferase" or demethylase or methylase or kinase or phosphatase or ubiquitin$ or ribosylase or protease	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L13	51801	fusion WITH (nucleot$ or protein or peptide)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L14	719	(chormatin or histone or nucleosome) with (modif$ or remodel$ or alter$ or reposit$)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:47
L15	11302	("zinc finger" or DNA) WITH "binding domain"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L16	200401	erythropoietin or androgen or PPAR or p15 or p16 or p53 or pRB or retinoblast$ or dystrophin or cadherin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L17	16	L7 and L11 and chromatin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L18	53132	(|536/23.1|536/23.4|536/24.1|435/325|435/254.2|435/320.1|530/300|530/350|435/183|530/402|.ccls.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L19	25482	L18 and L13	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L20	22781	L19 and L12	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L21	1527	(chromatin or histone or nucleosome) with (modif$ or remodel$ or alter$ or reposit$)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L22	300	L21 and L20	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L23	180	L22 and L15	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43

L24	127	L23 and L16	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L25	8	L24 and "chromatin remodeling complex"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L26	67	wolffe.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L27	33	L26 and "chromatin"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L28	10	"covalent modification" WITH (histone or chromatin or nucleosome)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L29	1339	"SAM synthetase" or HP1 or "su(var)" or "e(var"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L30	0	"wolffe.in"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L31	67	wolffe.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L32	9944	cox.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L33	67	wolffe.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L34	9944	cox.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L35	160	collingwood.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43

L36	506	sangamo$.as.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L37	143891	"methyl transferase" or demethylase or methylase or kinase or phosphatase or ubiquitin$ or ribosylase or protease	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:48
L38	51801	fusion WITH (nucleot$ or protein or peptide)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:47
L39	719	(chormatin or histone or nucleosome) with (modif$ or remodel$ or alter$ or reposit$)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L40	11302	("zinc finger" or DNA) WITH "binding domain"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L41	200401	erythropoietin or androgen or PPAR or p15 or p16 or p53 or pRB or retinoblast$ or dystrophin or cadherin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L42	53132	(|536/23.1|536/23.4|536/24.1|435/325|435/254.2|435/320.1|530/300|530/350|435/183|530/402|.ccls.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L43	25482	L42 and L38	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L44	22781	L43 and L37	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L45	1527	(chromatin or histone or nucleosome) with (modif$ or remodel$ or alter$ or reposit$)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L46	300	L45 and L44	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L47	180	L46 and L40	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43

L48	33	L26 and "chromatin"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L49	22	L32 and "zinc finger"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L50	6	"6453242".pn. or "6534261".pn. or "6503717".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L51	33	L33 and "chromatin"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L52	16	L33 and L36 and chromatin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L53	127	L47 and L41	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L54	8	L53 and "chromatin remodeling complex"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:47
L55	127	L47 and L41	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L56	69	L29 and L40	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L57	56	L56 and L38	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L58	2	"6534261".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43
L59	2	"6534261".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:43

L60	1527	(chromatin or histone or nucleosome) with (modif$ or remodel$ or alter$ or reposit$)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:47
L61	53490	fusion WITH (nucleot$ or protein or peptide or molecule or construct)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:48
L62	143891	"methyl transferase" or demethylase or methylase or kinase or phosphatase or ubiquitin$ or ribosylase or protease or de-ubiquitin$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:49
L63	651	l60 and l61 and l62	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:49
L64	455	l63 and "DNA binding"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:50
L65	14370	l61 SAME l62	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:50
L67	203	l65 and l60	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 11:51
L68	99	l67 and l15	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:24
L69	0	2003/0049649	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:22
L70	0	"2003/0049649"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:22
L71	2	"20030049649"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:23
L72	0	l71 and deubiquitin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:23

L73	1	l71 and ubiquitin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:23
L74	2	l68 and "ubiquitin hydrolase"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:25
L75	1	l68 and BAP1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:31
L76	1	l75 and BAP-1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:32
L77	1	l76 and (BAP-1 SAME fusion)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/07/01 12:32

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FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 10:56:55 ON 01 JUL 2005
L1       193584 S WOLFFE?/AU OR URNOV?/AU OR RASCHKE?/AU OR COLLINGWOOD?/AU OR
L2        57236 S FUSION (2W) (PROTEIN OR MOLECULE OR CONSTRUCT)
L3        99119 S "METHYLASE" OR "METHYLATION" OR "METHYL TRANSFERASE" OR "HIST
L4          235 S L2 (P) L3
L5            0 S L4 AND L1
L6          694 S L1 AND L3
L7            2 S L6 AND L2
L8            1 DUP REM L7 (1 DUPLICATE REMOVED)
L9           13 S L4 AND "DNA BINDING DOMAIN"
L10           5 DUP REM L9 (8 DUPLICATES REMOVED)
L11       15796 S (ENZYMATIC OR ENZYME) (2W) (SUBUNIT OR COMPONENT)
L12          16 S L11 (P) L3
L13           0 S L12 AND L2
L14           8 DUP REM L12 (8 DUPLICATES REMOVED)
L15           0 S L14 AND L1
L16         176 S SANGAMO?
L17           0 S L16 AND L11
L18        6388 S CHROMATIN (2W) (MODIFICATION OR REMODEL? OR ALTER?)
L19         970 S HISTONE (2W) (MODIFICATION OR REMODEL? OR ALTER?)
L20           8 S L18 AND L2 AND L3
L21           0 S L19 AND L2 AND L3
L22           6 DUP REM L20 (2 DUPLICATES REMOVED)
L23           8 S L18 AND L2 AND L3
L24          89 S L18 AND L2
L25          44 S L24 NOT PY>=2003
L26          23 DUP REM L25 (21 DUPLICATES REMOVED)
L27          11 S L26 AND (DBD OR "DNA BINDING")
L28         374 S L1 AND L2
L29           0 S L28 AND L18
L30           0 S L28 AND L19
L31           9 S L19 AND L2
L32           5 DUP REM L31 (4 DUPLICATES REMOVED)

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L8 ANSWER 1 OF 1 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2000221588 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10756192
TITLE: MeCP2 driven transcriptional repression in vitro: selectivity for methylated DNA, action at a distance and contacts with the basal transcription machinery.
AUTHOR: Kaludov N K; **Wolffe A P**
CORPORATE SOURCE: Laboratory of Molecular Embryology, National Institute of Child Heath and Human Development, NIH, Building 18T, Room 106, Bethesda, MD 20892-5431, USA.
SOURCE: Nucleic acids research, (2000 May 1) 28 (9) 1921-8. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000629
Last Updated on STN: 20010521
Entered Medline: 20000620

AB The pathways for selective transcriptional repression of methylated DNA templates by the methyl-CpG-binding protein MeCP2 have been investigated using a purified in vitro transcription system that does not assemble chromatin. MeCP2 selectively inhibits transcription complex assembly on methylated DNA but does not destabilize a pre-assembled transcription complex. MeCP2 functions to repress transcription at a distance of >500 bp from the transcription start site. The transcription repression domain (TRD) of MeCP2 will repress transcription in vitro when fused to a heterologous Gal4 DNA-binding domain. The TRD associates with TFIIB. Exogenous TFIIB does not relieve transcriptional repression established by either intact MeCP2 or a Gal4-TRD **fusion protein** under these in vitro conditions, nor does the addition of histone deacetylase inhibitors. We find that the transcriptional repression established by both MeCP2 and the Gal4-TRD **fusion protein** in vitro also correlates with selective assembly of large nucleoprotein complexes. The formation of such complexes reflects a local concentration of DNA-bound transcriptional repressor that may stabilize a state of repression even in the presence of exogenous transcriptional machinery.

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L10 ANSWER 1 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004501235 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15382263
TITLE: MLL/GRAF fusion in an infant acute monocytic leukemia (AML M5b) with a cytogenetically cryptic ins(5;11)(q31;q23q23).
AUTHOR: Panagopoulos Ioannis; Kitagawa Ashly; Isaksson Margareth; Morse Helena; Mitelman Felix; Johansson Bertil
CORPORATE SOURCE: Department of Clinical Genetics, University Hospital, SE-221 85 Lund, Sweden.. ioannis.panagopoulos@klingen.lu.se
SOURCE: Genes, chromosomes & cancer, (2004 Dec) 41 (4) 400-4. Journal code: 9007329. ISSN: 1045-2257.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20041008
Last Updated on STN: 20041219

AB More than 30 fusions involving the MLL gene at 11q23 have been reported in acute myeloid leukemia (AML). Some of these chimeras are rather common, such as MLL/MLLT3(AF9), but many are quite rare, with some, for example, MLL/GRAF, described only in a single case. The MLL/GRAF fusion, in which the reciprocal hybrid was not expressed, suggesting that the former transcript was the leukemogenic one, was detected in a juvenile myelomonocytic leukemia with a t(5;11)(q31;q23). Here, we report a second case--an infant acute monocytic leukemia (AML M5b)--with an MLL/GRAF fusion. By conventional G-banding, the karyotype was normal. However, Southern blot and fluorescence in situ hybridization analyses revealed that MLL was rearranged and that the 5' part of the MLL gene was inserted into 5q in the vicinity of 5q31, which harbors GRAF. Reverse-transcriptase polymerase chain reaction (PCR) showed that exon 9 of MLL was fused in-frame with exon 19 of GRAF. Extralong genomic PCR with subsequent sequence analysis demonstrated that the breakpoints occurred in intron 9 of MLL, nine base pairs (bp) downstream from exon 9, and in intron 18 of GRAF, 117 bp downstream from exon 18. A 6-bp insertion (ACACTC) of unknown origin was present at the junction. The putative MLL/GRAF **fusion protein** would retain the AT-hook **DNA-binding domain**, the DNA **methyl transferase** motif, the transcription repression domain of MLL, and the SH3 domain of GRAF. As expected, the reciprocal GRAF/MLL was neither expressed nor generated at the genomic level as a consequence of the ins(5;11)(q31;q23q23). On the basis of the now-reported two cases with MLL/GRAF, we conclude that this transcript--but not the reciprocal one--characterizes a rare genetic subgroup of infant AML.

L10 ANSWER 2 OF 5 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:167963 BIOSIS
DOCUMENT NUMBER: PREV200400161997
TITLE: The leukemia associated transcription factor AML1 interacts with SUV39H1 and is methylated in vivo.
AUTHOR(S): Sinha, Kislay K. [Reprint Author]; Chakraborty, Soumen [Reprint Author]; Senyuk, Vitalyi [Reprint Author]; Nucifora, Giuseppina [Reprint Author]
CORPORATE SOURCE: Pathology, University of Illinois at Chicago, Chicago, IL, USA
SOURCE: Blood, (November 16 2003) Vol. 102, No. 11, pp. 160b-161b. print.
Meeting Info.: 45th Annual Meeting of the American Society of Hematology. San Diego, CA, USA. December 06-09, 2003. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 24 Mar 2004
Last Updated on STN: 24 Mar 2004

AB Acute myeloid leukemia 1 (AML1) belongs to a highly conserved family of

transcription factors and is a key regulator of hematopoiesis. AML1 is located on human chromosome 21q22.12 and is the most frequently targeted gene in chromosomal translocations associated with acute myeloid leukemia (AML) and acute B-cell lymphoblastic leukemia (B-ALL). The most frequent rearrangements are t(8;21) found in about 15% of AML subtype M2 and t(12;21) associated with about 30% of B-ALL. These rearrangements result in the formation of fusion proteins. The high frequency of rearrangement indicates the critical role of AML1 in normal hematopoiesis. Here we report that AML1 physically interacts with histone **methyl transferase**, SUV39H1. The interacting region of AML1 is within the Runt domain, which is the **DNA-binding domain** of AML1. Immunofluorescence microscopy revealed that this interaction dissolves the net-like nuclear structure of AML1 and changes the distribution pattern of AML1 in the nucleus. We also show that AML1 is methylated in vivo, probably by a **methyl transferase** other than SUV39H1. To define the biological function of AML1/SUV39H1 interaction, we have analyzed the ability of AML1 to bind specifically to the MCSFR promoter in presence and absence of SUV39H1. Our data suggest that interaction with SUV39H1 decreases the ability of AML1 to bind to DNA. In reporter gene assay with MCSFR promoter, we observed that AML1 transactivity is reduced significantly with SUV39H1. It has been suggested that the oligomerization of AML-fusion proteins leads to abnormal recruitment of transcription co-regulators and to deregulation of AML1-dependent genes in leukemia. Because the Runt domain of AML1 is consistently conserved in all AML-fusion proteins, it is possible that the oligomerization of the **fusion protein** could result in recruitment of SUV39H1 and disruption of the normal equilibrium between AML1-bound and unbound SUV39H1 in the cells resulting in deregulation of hematopoietic genes.

L10 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 95189111 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7883193
TITLE: Overproduction, purification and structural characterization of the functional N-terminal **DNA -binding domain** of the fru repressor from Escherichia coli K-12.
AUTHOR: Scarabel M; Penin F; Bonod-Bidaud C; Negre D; Cozzone A J; Cortay J C
CORPORATE SOURCE: Institut de Biologie et Chimie des Proteines, C.N.R.S., Lyon, France.
SOURCE: Gene, (1995 Feb 3) 153 (1) 9-15.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950425
Last Updated on STN: 19980206
Entered Medline: 19950407

AB A DNA fragment encoding the **DNA-binding domain** (amino acids 1-60) of the Escherichia coli fru transcriptional regulator was cloned into the pGEX-KT vector and expressed in frame with the fused gene encoding glutathione S-transferase. The **fusion protein** was purified to homogeneity by affinity chromatography on immobilized glutathione, and then cleaved with thrombin. After separation by a cation-exchange chromatography step, the **DNA-binding domain** exhibited proper folding, as shown by proton NMR analysis. Furthermore, it showed specific interaction with the operator region of the ace operon, as checked by gel retardation and DNA **methylation**-protection experiments.

L10 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 92269842 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1588965
TITLE: Characterization of the DNA-binding activity of GCR1: in vivo evidence for two GCR1-binding sites in the upstream

activating sequence of TPI of Saccharomyces cerevisiae.
AUTHOR: Huie M A; Scott E W; Drazinic C M; Lopez M C; Hornstra I K; Yang T P; Baker H V
CORPORATE SOURCE: Department of Immunology and Medical Microbiology, University of Florida College of Medicine, Gainesville 32610-0266.
CONTRACT NUMBER: GM-4133 (NIGMS)
SOURCE: Molecular and cellular biology, (1992 Jun) 12 (6) 2690-700. Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920710
Last Updated on STN: 19980206
Entered Medline: 19920624

AB GCR1 gene function is required for high-level glycolytic gene expression in Saccharomyces cerevisiae. Recently, we suggested that the CTTCC sequence motif found in front of many genes encoding glycolytic enzymes lay at the core of the GCR1-binding site. Here we mapped the **DNA -binding domain** of GCR1 to the carboxy-terminal 154 amino acids of the polypeptide. DNase I protection studies showed that a hybrid MBP-GCR1 **fusion protein** protected a region of the upstream activating sequence of TPI (UASTPI), which harbored the CTTCC sequence motif, and suggested that the **fusion protein** might also interact with a region of the UAS that contained the related sequence CATCC. A series of in vivo G **methylation** protection experiments of the native TPI promoter were carried out with wild-type and gcr1 deletion mutant strains. The G doublets that correspond to the C doublets in each site were protected in the wild-type strain but not in the gcr1 mutant strain. These data demonstrate that the UAS of TPI contains two GCR1-binding sites which are occupied in vivo. Furthermore, adjacent RAP1/GRF1/TUF- and REB1/GRF2/QBP/Y-binding sites in UASTPI were occupied in the backgrounds of both strains. In addition, DNA band-shift assays were used to show that the MBP-GCR1 **fusion protein** was able to form nucleoprotein complexes with oligonucleotides that contained CTTCC sequence elements found in front of other glycolytic genes, namely, PGK, ENO1, PYK, and ADH1, all of which are dependent on GCR1 gene function for full expression. However, we were unable to detect specific interactions with CTTCC sequence elements found in front of the translational component genes TEF1, TEF2, and CRY1. Taken together, these experiments have allowed us to propose a consensus GCR1-binding site which is 5'-(T/A)N(T/C)N(G/A)NC(T/A)TCC(T/A)N(T/A)(T/A)(T/G)-3'.

L10 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 89231640 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2540961
TITLE: Expression of active hormone and DNA-binding domains of the chicken progesterone receptor in E. coli.
AUTHOR: Eul J; Meyer M E; Tora L; Bocquel M T; Quirin-Stricker C; Chambon P; Gronemeyer H
CORPORATE SOURCE: Laboratoire de Genetique Moleculaire des Eucaryotes du CNRS, Faculte de Medecine, Strasbourg, France.
SOURCE: EMBO journal, (1989 Jan) 8 (1) 83-90. Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198906
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890622

AB Bacterially-expressed fusion proteins containing the DNA-(region C) or hormone-binding (region E) domains of the chicken progesterone receptor (cPR) fused to the C terminus of Escherichia coli beta-galactosidase were

analysed for the specificity of interaction with natural and synthetic hormone-responsive elements (HREs) and progestins, respectively. The purified **fusion protein** containing the progestin-binding domain bound progesterone with an apparent Kd of 1.0-1.5 nM and was specifically photocross-linked with the synthetic progestin R5020 in crude bacterial lysates. Labelling of intact bacterial cells with [3H]R5020 revealed that the majority, if not all, of the bacterially produced hormone-binding domain was active. No differences in the binding to a synthetic palindromic glucocorticoid/progestin-responsive element (GRE/PRE) were found when the bacterially produced cPR **DNA-binding domain** was compared in **methylation** interference assays with the full-length chicken progesterone receptor form A expressed in eukaryotic cells. The study of dissociation kinetics, however, revealed differences in the half-life of the complexes formed between the palindromic GRE/PRE and either the receptor form A or the **fusion protein** containing the cPR **DNA-binding domain**. DNase I protection experiments demonstrated that the bacterially produced region C of the cPR generated specific 'footprints' on the mouse mammary tumour virus long terminal repeat (MMTV-LTR) which were nearly identical to those previously reported for the rat glucocorticoid receptor.

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L27 ANSWER 5 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2001534396 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11581372
TITLE: Adenovirus **DNA binding** protein interacts with the SNF2-related CBP activator protein (SrCap) and inhibits SrCap-mediated transcription.
AUTHOR: Xu X; Chackalaparampil I; Monroy M A; Cannella M T; Pesek E; Chrivia J; Yaciuk P
CORPORATE SOURCE: Department of Molecular Microbiology and Immunology, St. Louis University Health Sciences Center, St. Louis, Missouri 63104, USA.
CONTRACT NUMBER: CA-68066 (NCI)
SOURCE: Journal of virology, (2001 Nov) 75 (21) 10033-40.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011003
Last Updated on STN: 20011029
Entered Medline: 20011025

AB The SNF2-related CBP activator protein, SrCap (pronounced "sir cap"), shares homology with the SNF2/SWI2 protein family. SrCap was cloned through its ability to bind CBP. SrCap can function as a CBP coactivator and can activate transcription in a reporter assay when expressed as a Gal-SrCap **fusion protein**. A monoclonal antibody raised against the carboxyl terminus of SrCap coimmunoprecipitates CBP/p300, supporting the model that SrCap is a CBP binding protein and that these proteins can be found together in a cellular protein complex. In addition, several cellular proteins are coimmunoprecipitated by the SrCap-specific antibody. Since adenovirus E1A proteins interact with CBP/p300 proteins, we examined what proteins could be copurified in a SrCap-specific coimmunoprecipitation assay from lysates of adenovirus-infected cells. While E1A proteins were not detected in this complex, to our surprise, we observed the presence of an infected-cell-specific band of 72 kDa, which we suspected might be the adenovirus **DNA binding** protein, DBP. The adenovirus DBP is a multifunctional protein involved in several aspects of the adenovirus life cycle, including an ability to modulate transcription. The identity of DBP was confirmed by DBP-specific Western blot analysis and by reimmunoprecipitating DBP from denatured SrCap-specific protein complexes. Using in vitro-translated DBP and SrCap proteins, we demonstrated that these proteins interact. To determine whether this interaction could affect SrCap-mediated transcription, we tested whether increasing amounts of DBP could modulate the Gal-SrCap transcription activity. We observed that DBP inhibited Gal-SrCap transcription activity in a dose-dependent manner. These data suggest a novel mechanism of adenovirus host cell control by which DBP binds to and inactivates SrCap, a member of the SNF2 **chromatin-remodeling** protein family.

L27 ANSWER 6 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2001325909 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11313475
TITLE: A bipartite yeast SSRP1 analog comprised of Pob3 and Nhp6 proteins modulates transcription.
AUTHOR: Brewster N K; Johnston G C; Singer R A
CORPORATE SOURCE: Departments of Biochemistry & Molecular Biology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4H7.
SOURCE: Molecular and cellular biology, (2001 May) 21 (10) 3491-502.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20020919
Entered Medline: 20010607

AB The FACT complex of vertebrate cells, comprising the Cdc68 (Spt16) and SSRP1 proteins, facilitates transcription elongation on a nucleosomal template and modulates the elongation-inhibitory effects of the DSIF complex in vitro. Genetic findings show that the related yeast (Saccharomyces cerevisiae) complex, termed CP, also mediates transcription. The CP components Cdc68 and Pob3 closely resemble the FACT components, except that the C-terminal high-mobility group (HMG) box domain of SSRP1 is not found in the yeast homolog Pob3. We show here that Nhp6a and Nhp6b, small HMG box proteins with overlapping functions in yeast, associate with the CP complex and mediate CP-related genetic effects on transcription. Absence of the Nhp6 proteins causes severe impairment in combination with mutations impairing the Swi-Snf **chromatin-remodeling** complex and the DSIF (Spt4 plus Spt5) elongation regulator, and sensitizes cells to 6-azauracil, characteristic of elongation effects. An artificial SSRP1-like protein, created by fusing the Pob3 and Nhp6a proteins, provides both Pob3 and Nhp6a functions for transcription, and competition experiments indicate that these functions are exerted in association with Cdc68. This particular Pob3-Nhp6a **fusion protein** was limited for certain Nhp6 activities, indicating that its Nhp6a function is compromised. These findings suggest that in yeast cells the Cdc68 partners may be both Pob3 and Nhp6, functioning as a bipartite analog of the vertebrate SSRP1 protein.

L27 ANSWER 7 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2001236537 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11274403
TITLE: Analysis of transforming activity of human synovial sarcoma-associated chimeric protein SYT-SSX1 bound to **chromatin remodeling** factor hBRM/hSNF2 alpha.
AUTHOR: Nagai M; Tanaka S; Tsuda M; Endo S; Kato H; Sonobe H; Minami A; Hiraga H; Nishihara H; Sawa H; Nagashima K
CORPORATE SOURCE: Laboratory of Molecular and Cellular Pathology, Hokkaido University School of Medicine, N 15, W7, Kita-ku, Sapporo 060-8638, Japan.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2001 Mar 27) 98 (7) 3843-8. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

AB Human synovial sarcoma has been shown to exclusively harbor the chromosomal translocation t(X;18) that produces the chimeric gene SYT-SSX. However, the role of SYT-SSX in cellular transformation remains unclear. In this study, we have established 3Y1 rat fibroblast cell lines that constitutively express SYT, SSX1, and SYT-SSX1 and found that SYT-SSX1 promoted growth rate in culture, anchorage-independent growth in soft agar, and tumor formation in nude mice. Deletion of the N-terminal 181 amino acids of SYT-SSX1 caused loss of its transforming activity. Furthermore, association of SYT-SSX1 with the **chromatin remodeling** factor hBRM/hSNF2 alpha, which regulates transcription, was demonstrated in both SYT-SSX1-expressing 3Y1 cells and in the human synovial sarcoma cell line HS-SY-II. The binding region between the two molecules was shown to reside within the N-terminal 181 amino acids stretch (aa 1--181) of SYT-SSX1 and 50 amino acids (aa 156--205) of hBRM/hSNF2 alpha and we found that the overexpression of this binding region of hBRM/hSNF2 alpha significantly suppressed the anchorage-independent growth of SYT-SSX1-expressing 3Y1 cells. To analyze

the transcriptional regulation by SYT-SSX1, we established conditional expression system of SYT-SSX1 and examined the gene expression profiles. The down-regulation of potential tumor suppressor DCC was observed among 1,176 genes analyzed by microarray analysis, and semi-quantitative reverse transcription--PCR confirmed this finding. These data clearly demonstrate transforming activity of human oncogene SYT-SSX1 and also involvement of **chromatin remodeling** factor hBRM/hSNF2 alpha in human cancer.

L27 ANSWER 8 OF 11 MEDLINE on STN
ACCESSION NUMBER: 1999326293 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10397708
TITLE: **Chromatin remodeling** and leukemia: new therapeutic paradigms.
AUTHOR: Redner R L; Wang J; Liu J M
CORPORATE SOURCE: Division of Hematology/Oncology, Department of Medicine, University of Pittsburgh Medical Center, Pittsburgh, PA, USA.. redner+@pitt.edu
CONTRACT NUMBER: CA67346 (NCI)
SOURCE: Blood, (1999 Jul 15) 94 (2) 417-28. Ref: 149
Journal code: 7603509. ISSN: 0006-4971.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199908
ENTRY DATE: Entered STN: 19990816
Last Updated on STN: 19990816
Entered Medline: 19990805

L27 ANSWER 9 OF 11 MEDLINE on STN
ACCESSION NUMBER: 1998187598 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9528749
TITLE: SWI-SNF complex participation in transcriptional activation at a step subsequent to activator binding.
AUTHOR: Ryan M P; Jones R; Morse R H
CORPORATE SOURCE: Molecular Genetics Program, Wadsworth Center, New York State Department of Health, and State University of New York School of Public Health, Albany 12201-2002, USA.
CONTRACT NUMBER: GM51993 (NIGMS)
SOURCE: Molecular and cellular biology, (1998 Apr) 18 (4) 1774-82.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980529
Last Updated on STN: 19980529
Entered Medline: 19980521

AB The SWI-SNF complex in yeast and related complexes in higher eukaryotes have been implicated in assisting gene activation by overcoming the repressive effects of chromatin. We show that the ability of the transcriptional activator GAL4 to bind to a site in a positioned nucleosome is not appreciably impaired in swi mutant yeast cells. However, **chromatin remodeling** that depends on a transcriptional activation domain shows a considerable, although not complete, SWI-SNF dependence, suggesting that the SWI-SNF complex exerts its major effect at a step subsequent to activator binding. We tested this idea further by comparing the SWI-SNF dependence of a reporter gene based on the GAL10 promoter, which has an accessible upstream activating sequence and a nucleosomal TATA element, with that of a CYC1-lacZ reporter, which has a relatively accessible TATA element. We found that the GAL10-based reporter gene showed a much stronger SWI-SNF dependence than did the CYC1-lacZ reporter with several different activators. Remarkably, transcription of the GAL10-based reporter by a GAL4-GAL11

fusion protein showed a nearly complete requirement for the SWI-SNF complex, strongly suggesting that SWI-SNF is needed to allow access of TFIID or the RNA polymerase II holoenzyme. Taken together, our results demonstrate that **chromatin remodeling** in vivo can occur by both SWI-SNF-dependent and -independent avenues and suggest that the SWI-SNF complex exerts its major effect in transcriptional activation at a step subsequent to transcriptional activator-promoter recognition.

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ACCESSION NUMBER: 2003:356288 BIOSIS
DOCUMENT NUMBER: PREV200300356288
TITLE: PLZF Mediates Transcriptional Repression of Hox Gene Expression through **Chromatin Remodeling** and Recruitment of Polycomb Proteins.
AUTHOR(S): Barna, Maria [Reprint Author]; Merghoub, Taha [Reprint Author]; Costoya, Jose A. [Reprint Author]; Ruggero, Davide [Reprint Author]; Branford, Matthew [Reprint Author]; Pandolfi, Pier Paolo [Reprint Author]
CORPORATE SOURCE: Department of Pathology, Memorial Sloan-Kettering Cancer Center, New York, NY, USA
SOURCE: Blood, (November 16 2002) Vol. 100, No. 11, pp. Abstract No. 224. print.
Meeting Info.: 44th Annual Meeting of the American Society of Hematology. Philadelphia, PA, USA. December 06-10, 2002. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Aug 2003
Last Updated on STN: 6 Aug 2003

AB In APL, translocations between chromosome 11 and 17 fuse the PLZF gene to the RARalpha gene. The resulting oncogenic fusion proteins act as potent RA insensitive transcriptional repressors through aberrant recruitment of nuclear co-repressors and HDAC, rendering the APL blasts unresponsive to the differentiating effects of RA. Although RA can induce the degradation of the **fusion protein**, its repressive effect is maintained after RA treatment. The molecular mechanisms responsible for this epigenetic transcriptional silencing remain unknown as well as whether the dominant negative actions of the fusion proteins, on PLZF function, play a role in this process. In an attempt to identify target genes directly regulated by PLZF as well as to define the molecular basis for epigenetic gene silencing in APL, we have analyzed the ability of PLZF to regulate target Hox genes, which are aberrantly expressed in Plzf null mice. We show in knock-out and transgenic mice that PLZF acts in vivo to directly regulate the spatial expression of the AbdB HoxD gene complex by binding to regulatory elements required for restricted Hox gene expression and through recruitment of histone deacetylases. Furthermore, we demonstrate that PLZF co-localizes and physically interacts with Polycomb proteins (PcGs), which act to remodel chromatin epigenetically since they do not bind to DNA in a sequence specific manner. We demonstrate that PLZF directly tethers PcG **chromatin remodeling** activity on target **DNA binding** sites within Hox gene regulatory elements and that this interaction is essential for blocking Hox gene activation derived from posteriorizing signals in the developing embryos, such as RA. The fact that PcGs and PLZF physically interact may provide a mechanism underlying the aberrant repressive function of the oncogenic fusion proteins in APL. The recruitment of PcGs to the leukemogenic transcription complex may prevent proper transcriptional activation of RAR alpha target genes even in the absence of the **fusion protein**. In addition, these results directly implicate the deregulated function and/or expression of specific HOX genes in leukemogenesis.

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ACCESSION NUMBER: 2002:129878 BIOSIS
DOCUMENT NUMBER: PREV200200129878
TITLE: Reactivation of a silenced, methylated p16INK4a gene by low-dose 5-aza-2'-deoxycytidine requires activation of the p38 map kinase signal transduction pathway.
AUTHOR(S): Lavelle, Donald [Reprint author]; DeSimone, Joseph; Hankewych, Maria; Kousnetzova, Tatiana; Chen, Yi-Hsiang
CORPORATE SOURCE: Department of Medicine, University of Illinois at Chicago, Chicago, IL, USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 105a. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1. Orlando, Florida, USA. December 07-11, 2001. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002
AB DNA methylation silences the expression of multiple tumor supressor genes in many types of tumors by inducing repressive chromatin structures mediated by binding of methylated **DNA binding** (MBD) proteins associated with protein complexes containing histone deacetylase (HDAC) activity and **chromatin remodeling** factors. Treatment with the DNA demethylating drug 5-aza-2'-deoxycytidine (decitabine; DAC) reactivates the expression of silenced, methylated tumor suppressor genes by alleviating methylation-mediated repression. The synergistic reactivation of silenced, methylated genes by a combination of the HDAC inhibitor trichostatin A with low doses of DAC inducing limited demethylation demonstrated the important role of HDAC in the maintenance of methylation-mediated gene silencing (Cameron et al, Nat Genet 21:103, 1999). Whether DAC induces other activities that may be essential in the reactivation of silenced, methylated genes has not been investigated. Environmental and pharmacologic stress activates alternative map kinase signal tranduction pathways resulting in MSK 1-mediated phosphorylation of a minute fraction of histone H3 on serine 10. Phosphorylation of H3 increases sensitivity to hyperacetylation by HDAC inhibitors and histone acetyltransferases. Our objective in these experiments was to: 1) determine whether DAC treatment activated map kinase signal transduction pathways, and 2) investigate the role of map kinase pathways in the reactivation of silenced, methylated tumor suppressor genes. We observed that DAC treatment reactivated expression of a silenced, methylated p16INK4a gene in HS-Sultan cells in a dose-dependent manner (10-7 to 10-6 M). Phosphorylation of p38 map kinase was increased in a linear, dose-dependent manner at DAC concentrations ranging from 10-8 to 10-6 M. No activation of ERK 1/2 was observed. Increased phosphorylation of p38 was observed as early as 12 hours following drug addition. The ability of DAC to reactivate p16INK4a expression was inhibited by the p38 map kinase inhibitor SB203580 (10muM) at low doses (10-7 M) but not high doses (10-6 M) of DAC. The degree of inhibition was reduced with increasing DAC dose. The ERK 1/2 inhibitor PD098059 had no effect. Neither SB203580 or PD098059 affected cell growth and therefore the inhibition of p16INK4a reactivation was not due to inhibition of DAC incorporation into DNA H89 (10muM), at a concentration shown to preferentially inhibit MSK 1 (Thomson et al, EMBO J:4779, 1999), also inhibited reactivation of p16INK4a at low doses of DAC, suggesting that MSK 1-mediated histone H3 phosphorylation was required for p16INK4a reactivation. Our results demonstrate that activation of the p38 map kinase signal transduction pathway is required for reactivation of a silenced methylated p16INK4 gene by low dose DAC and suggest that this is due to the induction of an active chromatin configuration through phosphorylation of histone H3 by MSK 1. Therefore, reactivation of a silenced, methylated p16INK4a tumor suppressor gene at low doses of DAC requires both a reduction of DNA methylation density leading to loss of repressive MBDHDAC complexes and induction of an active chromatin configuration through the p38 map kinase signal transduction pathway.

L32 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2001327673 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11394910
TITLE: Rb-associated protein 46 (RbAp46) inhibits transcriptional transactivation mediated by BRCA1.
AUTHOR: Chen G C; Guan L S; Yu J H; Li G C; Choi Kim H R; Wang Z Y
CORPORATE SOURCE: Division of Growth Regulation, Department of Medicine, Beth Israel-Deaconess Medical Center, 330 Brookline Avenue, Boston, Massachusetts 02215, USA.
SOURCE: Biochemical and biophysical research communications, (2001 Jun 8) 284 (2) 507-14.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010716
Last Updated on STN: 20010716
Entered Medline: 20010712

AB The retinoblastoma suppressor (Rb)-associated protein 46 (RbAp46) is a member of the WD-repeat protein family and a component of the **histone** modifying and **remodeling** complexes. Previously, we demonstrated that RbAp46 is a potent growth inhibitor that can suppress the transformed phenotype of tumor cells. To explore the molecular mechanisms of RbAp46 function, we used RbAp46 as a bait in a yeast two-hybrid screening and found that RbAp46 interacts specifically with the C-terminal region of BRCA1 (the BRCT domain), a domain involved in the t transactivation activity of BRCA1. Coimmunoprecipitation assays demonstrated that the interaction of RbAp46 with BRCA1 requires the first two of the four Trp-Asp (WD)-repeats of RbAp46. We also showed that expression of RbAp46 represses the transactivation activity mediated by the BRCT/Gal4 **fusion protein** and inhibits the transactivation of the p21 promoter mediated by the full-length BRCA1. Interestingly, the association of BRCA1 and RbAp46 is disrupted in cells treated with DNA-damaging agents. These results suggest that RbAp46 may specifically interact with BRCA1 and modulate its transactivation activity in response to DNA damage.